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Sequence Listing was accepted.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2008; month=5; day=20; hr=16; min=33; sec=18; ms=784; ]

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Application No: 10528563 Version No: 20

### Input Set:

### **Output Set:**

**Started:** 2008-05-02 14:58:00.513  
**Finished:** 2008-05-02 14:58:06.479  
**Elapsed:** 0 hr(s) 0 min(s) 5 sec(s) 966 ms  
**Total Warnings:** 77  
**Total Errors:** 42  
**No. of SeqIDs Defined:** 89  
**Actual SeqID Count:** 89

**Input Set:**

**Output Set:**

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Error code	Error Description
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E 257	Invalid sequence data feature in <221> in SEQ ID (3)
E 257	Invalid sequence data feature in <221> in SEQ ID (3) This error has occurred more than 20 times, will not be displayed
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)
W 213	Artificial or Unknown found in <213> in SEQ ID (21)
W 213	Artificial or Unknown found in <213> in SEQ ID (22)
W 213	Artificial or Unknown found in <213> in SEQ ID (23)
W 213	Artificial or Unknown found in <213> in SEQ ID (24)
W 213	Artificial or Unknown found in <213> in SEQ ID (25)
W 213	Artificial or Unknown found in <213> in SEQ ID (26)
W 213	Artificial or Unknown found in <213> in SEQ ID (27)
W 213	Artificial or Unknown found in <213> in SEQ ID (28)
W 213	Artificial or Unknown found in <213> in SEQ ID (29)
W 213	Artificial or Unknown found in <213> in SEQ ID (30)
W 213	Artificial or Unknown found in <213> in SEQ ID (31)
W 213	Artificial or Unknown found in <213> in SEQ ID (32) This error has occurred more than 20 times, will not be displayed



SEQUENCE LISTING

<110> JONSON, LARS  
REHFELD, JENS F.  
JOHNSEN, ANDERS H.

<120> METHODS FOR INCREASING THE PRODUCTION OF A  
RECOMBINANT POLYPEPTIDE FROM A HOST CELL

<130> 030307-0256

<140> 10528563  
<141> 2005-10-11

<150> PCT/DK03/00609  
<151> 2003-09-19

<150> DK PA200201391  
<151> 2002-09-20

<160> 89

<170> PatentIn Ver. 3.3

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consensus sequence

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<222> (2)..(3)  
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<210> 2  
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consensus sequence

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Xaa  
20 25 30

Xaa Xaa Xaa Xaa Xaa Asn Ala Xaa Thr Xaa Xaa Xaa Xaa Xaa Thr  
35 40 45

<210> 3  
<211> 46  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Pitrilysin  
consensus sequence

<220>  
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Tyr Pro Xaa Leu Xaa Xaa Xaa  
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Xaa Xaa Xaa Xaa Xaa Asn Ala Xaa Thr Xaa Xaa Xaa Xaa Thr  
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<210> 4  
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Val Arg Lys Tyr Pro Val Gly Gly Ile Phe His Gly Tyr Glu Val Arg  
20 25 30

Arg Ile Leu Pro Val Pro Glu Leu Arg Leu Thr Ala Val Asp Leu Val  
35 40 45

His Ser Gln Thr Gly Ala Glu His Leu His Ile Asp Arg Asp Asp Lys  
50 55 60

Asn Asn Val Phe Ser Ile Ala Phe Lys Thr Asn Pro Pro Asp Ser Thr  
65 70 75 80

Gly Val Pro His Ile Leu Glu His Thr Thr Leu Cys Gly Ser Val Lys  
85 90 95

Tyr Pro Val Arg Asp Pro Phe Phe Lys Met Leu Asn Lys Ser Leu Ala  
100 105 110

Asn Phe Met Asn Ala Met Thr Gly Pro Asp Tyr Thr Phe Phe Pro Phe  
115 120 125

Ser Thr Thr Asn Pro Gln Asp Phe Ala Asn Leu Arg Gly Val Tyr Leu  
130 135 140

Asp Ser Thr Leu Asn Pro Leu Leu Lys Gln Glu Asp Phe Asp Gln Glu  
145 150 155 160

Gly Trp Arg Leu Glu His Lys Asn Ile Thr Asp Pro Glu Ser Asn Ile  
165 170 175

Val Phe Lys Gly Val Val Tyr Asn Glu Met Lys Gly Gln Ile Ser Asn  
180 185 190

Ala Asn Tyr Tyr Phe Trp Ser Lys Phe Gln Gln Ser Ile Tyr Pro Ser  
195 200 205

Leu Asn Asn Ser Gly Gly Asp Pro Met Lys Ile Thr Asp Leu Arg Tyr  
210 215 220

Gly Asp Leu Leu Asp Phe His His Lys Asn Tyr His Pro Ser Asn Ala

225 230 235 240  
Lys Thr Phe Thr Tyr Gly Asn Leu Pro Leu Val Asp Thr Leu Lys Gln  
245 250 255  
Leu Asn Glu Gln Phe Ser Gly Tyr Gly Lys Arg Ala Arg Lys Asp Lys  
260 265 270  
Leu Leu Met Pro Ile Asp Leu Lys Lys Asp Ile Asp Val Lys Leu Leu  
275 280 285  
Gly Gln Ile Asp Thr Met Leu Pro Pro Glu Lys Gln Thr Lys Ala Ser  
290 295 300  
Met Thr Trp Ile Cys Gly Ala Pro Gln Asp Thr Tyr Asp Thr Phe Leu  
305 310 315 320  
Leu Lys Val Leu Gly Asn Leu Leu Met Asp Gly His Ser Ser Val Met  
325 330 335  
Tyr Gln Lys Leu Ile Glu Ser Gly Ile Gly Leu Glu Phe Ser Val Asn  
340 345 350  
Ser Gly Val Glu Pro Thr Thr Ala Val Asn Leu Leu Thr Val Gly Ile  
355 360 365  
Gln Gly Val Ser Asp Ile Glu Ile Phe Lys Asp Thr Val Asn Asn Ile  
370 375 380  
Phe Gln Asn Leu Leu Glu Thr Glu His Pro Phe Asp Arg Lys Arg Ile  
385 390 395 400  
Asp Ala Ile Ile Glu Gln Leu Glu Leu Ser Lys Lys Asp Gln Lys Ala  
405 410 415  
Asp Phe Gly Leu Gln Leu Leu Tyr Ser Ile Leu Pro Gly Trp Thr Asn  
420 425 430  
Lys Ile Asp Pro Phe Glu Ser Leu Leu Phe Glu Asp Val Leu Gln Arg  
435 440 445  
Phe Arg Gly Asp Leu Glu Thr Lys Gly Asp Thr Leu Phe Gln Asp Leu  
450 455 460  
Ile Arg Lys Tyr Ile Val His Lys Pro Cys Phe Thr Phe Ser Ile Gln  
465 470 475 480  
Gly Ser Glu Glu Phe Ser Lys Ser Leu Asp Asp Glu Glu Gln Thr Arg  
485 490 495  
Leu Arg Glu Lys Ile Thr Ala Leu Asp Glu Gln Asp Lys Lys Asn Ile  
500 505 510  
Phe Lys Arg Gly Ile Leu Leu Gln Glu Lys Gln Asn Glu Lys Glu Asp  
515 520 525  
Leu Ser Cys Leu Pro Thr Leu Gln Ile Lys Asp Ile Pro Arg Ala Gly

530 535 540  
Asp Lys Tyr Ser Ile Glu Gln Lys Asn Asn Thr Met Ser Arg Ile Thr  
545 550 555 560  
Asp Thr Asn Gly Ile Thr Tyr Val Arg Gly Lys Arg Leu Leu Asn Asp  
565 570 575  
Ile Ile Pro Phe Glu Leu Phe Pro Tyr Leu Pro Leu Phe Ala Glu Ser  
580 585 590  
Leu Thr Asn Leu Gly Thr Thr Glu Ser Phe Ser Glu Ile Glu Asp  
595 600 605  
Gln Ile Lys Leu His Thr Gly Gly Ile Ser Thr His Val Glu Val Thr  
610 615 620  
Ser Asp Pro Asn Thr Thr Glu Pro Arg Leu Ile Phe Gly Phe Asp Gly  
625 630 635 640  
Trp Ser Leu Asn Ser Lys Thr Asp His Ile Phe Glu Phe Trp Ser Lys  
645 650 655  
Ile Leu Leu Glu Thr Asp Phe His Lys Asn Ser Asp Lys Leu Lys Val  
660 665 670  
Leu Ile Arg Leu Leu Ala Ser Ser Asn Thr Ser Ser Val Ala Asp Ala  
675 680 685  
Gly His Ala Phe Ala Arg Gly Tyr Ser Ala Ala His Tyr Arg Ser Ser  
690 695 700  
Gly Ala Ile Asn Glu Thr Leu Asn Gly Ile Glu Gln Leu Gln Phe Ile  
705 710 715 720  
Asn Arg Leu His Ser Leu Leu Asp Asn Glu Glu Thr Phe Gln Arg Glu  
725 730 735  
Val Val Asp Lys Leu Thr Glu Leu Gln Lys Tyr Ile Val Asp Thr Asn  
740 745 750  
Asn Met Asn Phe Phe Ile Thr Ser Asp Ser Asp Val Gln Ala Lys Thr  
755 760 765  
Val Glu Ser Gln Ile Ser Lys Phe Met Glu Arg Leu Pro His Gly Ser  
770 775 780  
Cys Leu Pro Asn Gly Pro Lys Thr Ser Asp Tyr Pro Leu Ile Gly Ser  
785 790 795 800  
Lys Cys Lys His Thr Leu Ile Lys Phe Pro Phe Gln Val His Tyr Thr  
805 810 815  
Ser Gln Ala Leu Leu Gly Val Pro Tyr Thr His Lys Asp Gly Ser Ala  
820 825 830  
Leu Gln Val Met Ser Asn Met Leu Thr Phe Lys His Leu His Arg Glu

835                    840                    845  
Val Arg Glu Lys Gly Gly Ala Tyr Gly Gly Ala Ser Tyr Ser Ala  
850                    855                    860  
  
Leu Ala Gly Ile Phe Ser Phe Tyr Ser Tyr Arg Asp Pro Gln Pro Leu  
865                    870                    875                    880  
  
Lys Ser Leu Glu Thr Phe Lys Asn Ser Gly Arg Tyr Ile Leu Asn Asp  
885                    890                    895  
  
Ala Lys Trp Gly Val Thr Asp Leu Asp Glu Ala Lys Leu Thr Ile Phe  
900                    905                    910  
  
Gln Gln Val Asp Ala Pro Lys Ser Pro Lys Gly Glu Gly Val Thr Tyr  
915                    920                    925  
  
Phe Met Ser Gly Val Thr Asp Asp Met Lys Gln Ala Arg Arg Glu Gln  
930                    935                    940  
  
Leu Leu Asp Val Ser Leu Leu Asp Val His Arg Val Ala Glu Lys Tyr  
945                    950                    955                    960  
  
Leu Leu Asn Lys Glu Gly Val Ser Thr Val Ile Gly Pro Gly Ile Glu  
965                    970                    975  
  
Gly Lys Thr Val Ser Pro Asn Trp Glu Val Lys Glu Leu  
980                    985  
  
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<213> Schizosaccharomyces pombe  
  
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Thr His Asn Cys Arg Leu Phe Gln Arg Trp Leu His Val Gly Asp Lys  
20                    25                    30  
  
Val His Asp Phe Arg Val Val Asp Thr Lys Lys Val Pro Glu Leu Gln  
35                    40                    45  
  
Leu Asn Tyr Thr Arg Leu Lys His Glu Pro Thr Asn Ala Asp Met Ile  
50                    55                    60  
  
His Leu Asp Arg Glu Asp Pro Asn Ser Val Phe Ser Ile Gly Phe Gln  
65                    70                    75                    80  
  
Thr Pro Ala Glu Asn Asp Glu Gly Ile Pro His Ile Leu Glu His Thr  
85                    90                    95  
  
Thr Leu Cys Gly Ser Asn Lys Tyr Pro Val Arg Asp Pro Phe Phe Lys  
100                    105                    110

Met Leu Asn Arg Ser Leu Ala Thr Phe Met Asn Ala Phe Thr Ala Ser  
115 120 125

Asp Phe Thr Phe Tyr Pro Phe Ala Thr Val Asn Thr Thr Asp Tyr Lys  
130 135 140

Asn Leu Arg Asp Val Tyr Leu Asp Ala Thr Leu Phe Pro Lys Leu Arg  
145 150 155 160

Lys Leu Asp Phe Leu Gln Glu Gly Trp Arg Phe Glu His Ala Asp Val  
165 170 175

Asn Asp Lys Lys Ser Pro Ile Ile Phe Asn Gly Val Val Tyr Asn Glu  
180 185 190

Met Lys Gly Gln Val Ser Asp Ser Ser Tyr Ile Phe Tyr Met Leu Phe  
195 200 205

Gln Gln His Leu Phe Gln Gly Thr Ala Tyr Gly Phe Asn Ser Gly Gly  
210 215 220

Asp Pro Leu Ala Ile Pro Asp Leu Lys Tyr Glu Glu Leu Val Lys Phe  
225 230 235 240

His Arg Ser His Tyr His Pro Ser Asn Ala Lys Ile Leu Ser Tyr Gly  
245 250 255

Ser Phe Pro Leu Glu Asp Asn Leu Ser Ala Leu Ser Glu Thr Phe Arg  
260 265 270

Pro Phe Ser Lys Arg Glu Leu Asn Leu Pro Asn Thr Phe Leu Lys Glu  
275 280 285

Phe Asp Gln Glu Lys Arg Val Val Glu Tyr Gly Pro Leu Asp Pro Val  
290 295 300

Met Ala Pro Gly Arg Gln Val Lys Thr Ser Ile Ser Phe Leu Ala Asn  
305 310 315 320

Asp Thr Ser Asn Val Tyr Glu Thr Phe Ala Leu Lys Val Leu Ser Lys  
325 330 335

Leu Cys Phe Asp Gly Phe Ser Ser Pro Phe Tyr Lys Ala Leu Ile Glu  
340 345 350

Ser Gly Leu Gly Thr Asp Phe Ala Pro Asn Ser Gly Tyr Asp Ser Thr  
355 360 365

Thr Lys Arg Gly Ile Phe Ser Val Gly Leu Glu Gly Ala Ser Glu Glu  
370 375 380

Ser Leu Ala Lys Ile Glu Asn Leu Val Tyr Ser Ile Phe Asn Asp Leu  
385 390 395 400

Ala Leu Lys Gly Phe Glu Asn Glu Lys Leu Glu Ala Ile Leu His Gln  
405 410 415

Met Glu Ile Ser Leu Lys His Lys Ser Ala His Phe Gly Ile Gly Leu  
420 425 430

Ala Gln Ser Leu Pro Phe Asn Trp Phe Asn Gly Ala Asp Pro Ala Asp  
435 440 445

Trp Leu Ser Phe Asn Lys Gln Ile Glu Trp Leu Lys Gln Lys Asn Ser  
450 455 460

Asp Gly Lys Leu Phe Gln Lys Leu Ile Lys Lys Tyr Ile Leu Glu Asn  
465 470 475 480

Lys Ser Arg Phe Val Phe Thr Met Leu Pro Ser Ser Thr Phe Pro Gln  
485 490 495

Arg Leu Gln Glu Ala Glu Ala Lys Lys Leu Gln Glu Arg Thr Ser Lys  
500 505 510

Leu Thr Asp Glu Asp Ile Ala Glu Ile Glu Lys Thr Ser Val Lys Leu  
515 520 525

Leu Glu Ala Gln Ser Thr Pro Ala Asp Thr Ser Cys Leu Pro Thr Leu  
530 535 540

Ser Val Ser Asp Ile Pro Glu Thr Ile Asp Glu Thr Lys Leu Lys Phe  
545 550 555 560

Leu Asp Ile Ala Gly Met Lys Ala Gln Trp Tyr Asp Leu Ala Ala Gly  
565 570 575

Leu Thr Tyr Ile Arg Leu Leu Leu Pro Leu Lys Asn Phe Pro Glu Ser  
580 585 590

Leu Ile Pro Tyr Leu Pro Val Tyr Cys Asp Ala Cys Leu Asn Leu Gly  
595 600 605

Thr His Ser Glu Ser Ile Gly Asp Leu Glu His Gln Ile Arg Arg Tyr  
610 615 620

Thr Gly Gly Ile Ser Ile Ser Pro Ser Ala Val Thr Asn Asn Ser Asp  
625 630 635 640

Val Ser Lys Tyr Glu Leu Gly Ile Ala Ile Ser Gly Tyr Ala Leu Asp  
645 650 655

Lys Asn Val Gly Lys Leu Val Glu Leu Ile Asn Lys Ala Phe Trp Asn  
660 665 670

Thr Asn Leu Ser Asn Thr Asp Lys Leu Ala Ile Met Leu Lys Thr Ser  
675 680 685

Val Ser Gly Ile Thr Asp Gly Ile Ala Glu Lys Gly His Ser Phe Ala  
690 695 700

Lys Val Ser Ser Ala Ser Gly Leu Thr Glu Lys Thr Ser Ile Thr Glu  
705 710 715 720

Gln Leu Gly Gly Leu Thr Gln Val Lys Leu Leu Ser Gln Leu Ser Arg  
725 730 735

Glu Glu Ser Phe Gly Pro Leu Val Glu Lys Leu Thr Ala Ile Arg Glu  
740